now abandoned, which is a continuation-in-part of U.S. Patent Application No. 07/355,027, filed May 19, 1989, pending, all of which are incorporated by reference herein.

On page 9, please replace the paragraph beginning on line 8 with the following amended paragraph:

Figure 32 shows results of amino terminal amino acid sequencing of peptides (SEQ ID No.: 2, SEQ ID No.: 3, SEQ ID No.: 4, SEQ ID No.: 5) of the SDS PAGE bands 1, 2, and 3 that were generated by plasmin digestion of CHO-derived human MI.

On page 97, please replace the paragraph beginning on line 1 with the following amended paragraph:

The apparent size of peptide 3 by SDS-PAGE (14.5 kDal; Figure 31) suggests that it contains about 130-135 amino acids. Since it retains the N-terminal region, it would correspond to amino acids 1-130/135 of MI. By SDS-PAGE using gels with high percentage acrylamide, a small (2.5 kDal) fragment could be visualized in plasmin digests of MI. This fragment had the N-terminal sequence (Cys)-Pro-Met-Ile-Pro-(Cys)-Tyr-Ile-Ser-Ser-Pro-Xaa-Glu- (SEQ ID No: 1), i.e., it starts at residue 133 of MI (see Figure 2), and results from cleavage by plasmin of the bond between Arg 132 and Cys 133. It is likely that the 2.5 kDal fragment extends to residue Arg 170, and that after plasmin treatment under non-reducing conditions, the fragment representing amino acids 171-194 remains attached to the 1-132 fragment via a disulfide bond between Cys 128 and Cys 175. This suggestion is based on the likelihood that human MI has the same disulfide structure as human TIMP [Williamson et al., Biochem. J. 268, 267-274 (1990)]. The theoretical disulfide structure for human MI is shown in linearized fashion

LAW OFFICES
FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000